WHAT IS CLAIMED IS:

1.   A homology analysis system for analyzing
whether an analysis target data group is similar to
a first data group or a second data group wherein the
first and second data groups is different from the
analysis target data group, comprising:

a first homology value calculation unit
calculating a first homology value $\underline{x}$ representing a
homology between data included in the analysis target
data group and the first data group respectively,
wherein the first homology value calculating unit
sets $\underline{n}$ thresholds E each indicating a determination
criterion for the presence/absence of a homology and
calculates a first homology value x_i (i = 1, 2, $\cdots$, n)
for each threshold E_i;

a second homology value calculation unit
calculating a second homology value $\underline{y}$ representing a
homology between data included in the analysis target
data group and the second data group respectively,
wherein the second homology value calculating unit
sets $\underline{n}$ thresholds E each indicating a determination
criterion for the presence/absence of a homology and
calculates a second homology value y_i (i = 1, 2, $\cdots$, n)
for each threshold E_i; and

homology determination unit determining to which
one of the first and second data groups the analysis
target data group is similar on the basis of a

relationship between the first homology value x_i, the second homology value y_i, and the number n of thresholds.

2. A homology analysis system according to claim 1, wherein

the first homology value calculation unit determines the presence of a homology if a homology between data included in the analysis target data group and the first data group, respectively, is not less than the threshold E, and calculates the number of data having homologies as the first homology value x, and

the second homology value calculation unit determines the presence of a homology if a homology between data included in the analysis target data group and the second data group, respectively, is not less than the threshold E, and calculates the number of data having homologies as the second homology value y.

3. A homology analysis system according to claim 1, wherein

when the first data group has n_A data, and the second data group has n_B data,

the first homology value calculation unit calculates a first homology value x_{ij} ($j = 1, 2, \cdots, n_A$) for each data of the first data group with respect to one threshold E_i, and calculates a mean value $x_{i\_}$ of the calculated first homology values x_i with respect to the threshold E_i,

the second homology value calculation unit
calculates a second homology value y_{ij} (j = 1, 2, $\cdots$,
n_B) for each data of the second data group with respect
to one threshold E_i, and calculates a mean value $y_{i\_}$ of
the calculated second homology values y_i with respect
to the threshold E_i, and

the homology determination unit calculates
a homology determination value $Z_i{}^{(1)}$ indicating
similarity to one of the first data group and the
second data group according to

$$Z_i^{(1)} = \frac{\overline{X_i} - \overline{Y_i}}{u_i} \cdot \sqrt{\frac{n_A \cdot n_B}{n_A + n_B}} \qquad (\text{i} \qquad = \qquad 1, 2, \dots, n)$$

when

$$u_i = \sqrt{\frac{1}{n_A + n_B - 2}\left\{\sum_{j=1}^{n_A}(x_{ij} - \overline{X_i})^2 + \sum_{k=1}^{n_B}(y_{ik} - \overline{Y_i})^2\right\}}$$

4. A homology analysis system according to
claim 1, wherein

when the first data group has n_A data, and the
second data group has n_B data,

the first homology value calculation unit
calculates a first homology value x_{ij} (j = 1, 2, $\cdots$,
n_A) for each data of the first data group with respect
to one threshold E_i, and calculates a mean value $x_{i\_}$ of
the calculated first homology values x_i with respect to
the threshold E_i,

the second homology value calculation unit
calculates a second homology value y_{ij} (j = 1, 2, $\cdots$,

n_B) for each data of the second data group with respect to one threshold E_i, and calculates a mean value $\overline{y_i}$ of the calculated second homology values y_i with respect to the threshold E_i,

the homology determination unit calculates a homology determination value $Z_i^{(1)}$ indicating similarity to one of the first data group and the second data group according to

$$Z_i^{(1)} = \frac{\overline{x_i} - \overline{y_i}}{u_i} \cdot \sqrt{\frac{n_A \cdot n_B}{n_A + n_B}} \qquad (i \quad = \quad 1,2,...,n)$$

when

$$u_i = \sqrt{\frac{1}{n_A + n_B - 2}\left\{\sum_{j=1}^{nA}(x_{ij} - \overline{x_i})^2 + \sum_{k=1}^{nB}(y_{ik} - \overline{y_i})^2\right\}}$$

and

the homology analysis system further comprises determination result derivation unit determining that the analysis target data group has many data having homologies with the first data group, if the homology determination value $Z_i^{(1)}$ is larger than $t_\alpha(0, 10)$ wherein the homology determination value $Z_i^{(1)}$ is in accordance with a t-distribution and α is a degree of freedom.

5. A homology analysis system according to claim 1, in which

when the first data group has n_A data, and the second data group has n_B data,

the first homology value calculation unit calculates a first homology value x_{ij} (j = 1, 2, $\cdots$, n_A) for each data of the first data group with respect to one threshold E_i, and calculates a mean value $x_{i\_}$ of

5 the calculated first homology values x_i with respect to the threshold E_i,

the second homology value calculation unit calculates a second homology value y_{ij} (j = 1, 2, $\cdots$, n_B) for each data of the second data group with respect

10 to one threshold E_i, and calculates a mean value $y_{i\_}$ of the calculated second homology values y_i with respect to the threshold E_i,

the homology determination unit calculates a homology determination value $z_i^{(1)}$ indicating

15 similarity to one of the first data group and the second data group according to

$$ z_i^{(1)} = \frac{\overline{x_i} - \overline{y_i}}{u_i} \cdot \sqrt{\frac{n_A \cdot n_B}{n_A + n_B}} \qquad (i \quad = \quad 1, 2, \ldots, n) $$

when

$$ u_i = \sqrt{\frac{1}{n_A + n_B - 2} \left\{ \sum_{j=1}^{n_A} (x_{ij} - \overline{x_i})^2 + \sum_{k=1}^{n_B} (y_{ik} - \overline{y_i})^2 \right\}} $$

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and

the homology analysis system further comprises determination result derivation unit determining that the analysis target data group has many data having

25 homologies with the second data group, if the homology determination value $z_i^{(1)}$ is smaller than $-t_\alpha(0, 10)$

wherein the homology determination value $z_i{}^{(1)}$ is in accordance with a t-distribution and α is a degree of freedom.

6. A homology analysis system according to claim 4, wherein the determination result derivation unit further comprises homology validity determination unit calculating a homology validity determination value $Z^{(2)}$ given by

$$Z^{(2)} = \frac{|\overline{Z^{(1)}}| - t_{n_A + n_B - 2}(0.10)}{s / \sqrt{(n-1)}}$$

where $\underline{s}$ is a standard deviation of $z_i{}^{(1)}$ and $z_i{}^{(1)}\_$ is a mean value of $z_i{}^{(1)}$, and determining that the homology determination value $z_i{}^{(1)}$ is an invalid value, if the homology validity determination value $Z^{(2)}$ is less than a predetermined value $t_{n-1}(0, 10)$.

7. A homology analysis system according to claim 5, wherein the determination result derivation unit further comprises homology validity determination unit calculating a homology validity determination value $Z^{(2)}$ given by

$$Z^{(2)} = \frac{|\overline{Z^{(1)}}| - t_{n_A + n_B - 2}(0.10)}{s / \sqrt{(n-1)}}$$

where $\underline{s}$ is a standard deviation of $z_i{}^{(1)}$ and $z_i{}^{(1)}\_$ is a mean value of $z_i{}^{(1)}$, and determining that the homology determination value $z_i{}^{(1)}$ is an invalid value, if the homology validity determination value $Z^{(2)}$ is

less than a predetermined value $t_{n-1}(0, 10)$.

8. A homology analysis system according to claim 6, wherein the degree of freedom α is $n_A + n_B - 2$.

9. A homology analysis system according to claim 7, wherein the degree of freedom α is $n_A + n_B - 2$.

10. A homology analysis system according to claim 1, wherein the first and second homology value calculation unit calculates the homology values x_i and y_i by a BLAST method.

11. A homology analysis system according to claim 1, wherein the analysis target data group, the first data group, and the second data group are data representing gene sequences.

12. A homology analysis method of analyzing whether an analysis target data group is similar to a first data group or a second data group wherein the first and second data groups is different from the analysis target data group, comprising:

calculating a first homology value $\underline{x}$ representing a homology between data included in the analysis target data group and the first data group, respectively, wherein the calculating the first homology value $\underline{x}$ includes setting $\underline{n}$ thresholds E each indicating a determination criterion for the presence/absence of a homology and calculating the first homology value $\underline{x}$

as a first homology value x_i (i = 1, 2, ···, n) for each

threshold E_i;

calculating a second homology value $\underline{y}$ representing

a homology between data included in the analysis target

5   data group and the second data group, respectively,

wherein the calculating the second homology value $\underline{y}$

includes setting $\underline{n}$ thresholds E each indicating

a determination criterion for the presence/absence of

a homology and calculating the second homology value $\underline{y}$

10   as a second homology value y_i (i = 1, 2, ···, n) for

each threshold E_i; and

determining to which one of the first and second

data groups the analysis target data group is similar

on the basis of a relationship between the first

15   homology value x_i, the second homology value y_i, and

the number $\underline{n}$ of thresholds.

13.   A homology analysis program product causing

a computer system to analyze whether an analysis target

data group is similar to a first data group or a second

20   data group wherein the first and second data groups is

different from the analysis target data group,

comprising:

a recording medium;

a first program code which is recorded on the

25   ˙recording medium and gives the computer system a first

command for calculating a first homology value $\underline{x}$

representing a homology between data included in the

analysis target data group and the first data group, respectively, wherein the first command includes setting n thresholds E each indicating a determination criterion for the presence/absence of a homology and

5   calculating a first homology value x_i (i = 1, 2, $\cdots$, n) for each threshold E_i;

a second program code which is recorded on the recording medium and gives the computer system a second command for calculating a second homology value y

10   representing a homology between data included in the analysis target data group and the second data group, respectively, wherein the second command includes setting n thresholds E each indicating a determination criterion for the presence/absence of a homology and

15   calculating a second homology value y_i (i = 1, 2, $\cdots$, n) for each threshold E_i; and

a third program code which is recorded on the recording medium and gives the computer system a third command for determining to which one of the first and

20   second data groups the analysis target data group is similar on the basis of a relationship between the first homology value x_i, the second homology value y_i, and a number n of thresholds.

14. A transaction establishment system for

25   analyzing whether a transaction condition including at least two transaction condition data of a first transaction party is similar to a transaction condition

including at least two transaction conditions presented
by any one of at least two second transaction parties
to determine establishment of a transaction, thereby
determining whether a transaction is established
between the first transaction party and at least the
two second transaction parties, comprising:

a first homology value calculation unit
calculating a first homology value $\underline{x}$ representing a
homology between the transaction condition data of the
first transaction party and the transaction condition
data of one of the second transaction parties, wherein
the first homology value calculating unit sets $\underline{n}$
thresholds E each indicating a determination criterion
for the presence/absence of a homology and calculates
a first homology value x_i (i = 1, 2, $\cdots$, n) for each
threshold E_i; and

a second homology value calculation unit
calculating a second homology value $\underline{y}$ representing
a homology between at least two transaction condition
data of the first transaction party and transaction
condition data of the other party who is not a target
for which the first homology value calculation unit
performed homology value calculation, wherein the
second homology value calculating unit sets $\underline{n}$
thresholds E each indicating a determination criterion
for the presence/absence of a homology and calculates
a second homology value y_i (i = 1, 2, $\cdots$, n) for each

threshold E_i,

wherein the establishment of the transaction is determined on the basis of the first homology value x_i and the second homology value y_i.

5   15. A transaction establishment system according to claim 14, further comprising transaction establishment determination unit determining to which the transaction condition presented by any one of the second transaction parties the transaction condition of 10   the first transaction party is similar on the basis of a relationship between the first homology value x_i, the second homology value y_i, and a number $\underline{n}$ of thresholds.

16. A transaction establishment system according to claim 14, wherein

15   one transaction condition data of the first transaction party is made to correspond to one transaction condition data of the second transaction party, and

the first homology value calculation unit and 20   the second homology value calculation unit calculate homology values between transaction condition data which are made to correspond to each other.

17. A transaction establishment system according to claim 15, wherein

25   one transaction condition data of the first transaction party is made to correspond to one transaction condition data of the second transaction

party, and

the first homology value calculation unit and the second homology value calculation unit calculate homology values between transaction condition data which are made to correspond to each other.

18. A transaction establishment system according to claim 15, wherein the transaction establishment unit derives in order of similarity the second transaction party who has presented a transaction condition similar to a transaction condition of the first transaction party on the basis of a relationship between the first homology value x_i, the second homology value y_i, and the number $\underline{n}$ of thresholds.